AMENDMENTS TO THE CLAIMS

In the Claims:

Please amend claims 55-57

Claims 1-54 were previously cancelled

1-54. **(Cancelled)**

55. **(Currently amended)** A method for preparing lysine by cultivating a genetically modified *Corynebacterium glutamicum* comprising ~~microorganism, wherein the genetically modified microorganism comprises~~

(1) a nucleic acid molecule having promoter activity, wherein the nucleic acid molecule consists of ~~is selected from the group consisting of:~~

~~a)~~ a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1;

~~b) a nucleic acid molecule comprising a nucleotide sequence of at least 90% identity to the nucleotide sequence of SEQ ID NO:1;~~

~~c) a nucleic acid molecule which hybridizes with the complement of the nucleotide sequence of SEQ ID NO:1; and~~

~~d) a nucleic acid molecule comprising a fragment of the nucleic acid molecule of (a), (b) or (c);~~ or

(2) an expression unit comprising either

a) the nucleic acid molecule of ~~any one of~~ 1**[[**(a)-(d)**]]** wherein said nucleic acid molecule is functionally linked to a nucleic acid sequence which ensures the translation of ribonucleic acids, or

b) the nucleic acid molecule of SEQ ID NO:2;

wherein the nucleic acid molecule of (1) or the expression unit of (2) alters, regulates or causes the expression of at least one endogenous gene, compared with the wild type;

and wherein the at least one endogenous gene is selected from the group consisting of nucleic acids encoding an aspartate kinase, nucleic acids encoding an aspartate-semialdehyde dehydrogenase, nucleic acids encoding a diaminopimelate dehydrogenase, nucleic acids encoding a diaminopimelate decarboxylase, nucleic acids encoding a dihydrodipicolinate synthetase, nucleic acids encoding a dihydrodipicolinate reductase, nucleic acids encoding a glyceraldehyde-3-phosphate dehydrogenase, nucleic acids encoding a 3-phosphoglycerate

kinase, nucleic acids encoding a pyruvate carboxylase, nucleic acids encoding a triosephosphate isomerase, nucleic acids encoding a transcriptional regulator LuxR, nucleic acids encoding a transcriptional regulator LysR1, nucleic acids encoding a transcriptional regulator LysR2, nucleic acids encoding a malate-quinone oxidoreductase, nucleic acids encoding a glucose-6-phosphate dehydrogenase, nucleic acids encoding a 6-phosphogluconate dehydrogenase, nucleic acids encoding a transketolase, nucleic acids encoding a transaldolase, nucleic acids encoding a lysine exporter, nucleic acids encoding a biotin ligase, nucleic acids encoding an arginyl-tRNA synthetase, nucleic acids encoding a phosphoenolpyruvate carboxylase, nucleic acids encoding a fructose-1,6-bisphosphatase, nucleic acids encoding a protein OpcA, nucleic acids encoding a 1-phosphofructokinase and nucleic acids encoding a 6-phosphofructokinase.

56. **(Currently Amended)** The method of claim 55, wherein the genetically modified *Corynebacterium glutamicum* ~~microorganism~~ has an increased activity, as compared with the wild type, of at least one activity selected from the group consisting of aspartate kinase activity, aspartate-semialdehyde dehydrogenase activity, diaminopimelate dehydrogenase activity, diaminopimelate decarboxylase activity, dihydrodipicolinate synthetase activity, dihydrodipicolinate reductase activity, glyceraldehyde-3-phosphate dehydrogenase activity, 3-phosphoglycerate kinase activity, pyruvate carboxylase activity, triosephosphate isomerase activity, activity of the transcriptional regulator LuxR, activity of the transcriptional regulator LysR1, activity of the transcriptional regulator LysR2, malate-quinone oxidoreductase activity, glucose-6-phosphate deydrogenase activity, 6-phosphogluconate dehydrogenase activity, transketolase activity, transaldolase activity, lysine exporter activity, arginyl-tRNA synthetase activity, phosphoenolpyruvate carboxylase activity, fructose-1,6-bisphosphatase activity, protein OpcA activity, 1-phosphofructokinase activity, 6-phosphofructokinase activity and biotin ligase activity.

57. **(Currently Amended)** The method of claim 55 or 56, wherein the genetically modified *Corynebacterium glutamicum* ~~microorganism~~ has a reduced activity, as compared with the wild type, of at least one activity selected from the group consisting of threonine dehydratase activity, homoserine O-acetyltransferase activity, O-acetylhomoserine sulfhydrylase activity, phosphoenolpyruvate carboxykinase activity, pyruvate oxidase activity, homoserine kinase

activity, homoserine dehydrogenase activity, threonine exporter activity, threonine efflux protein activity, asparaginase activity, aspartate decarboxylase activity and threonine synthase activity.

58. **(Previously Presented)** The method of claim 55 or 56, wherein the lysine is isolated from the cultivation medium.

59. **(Previously Presented)** The method of claim 58, wherein the lysine is purified.

60. **(Previously Presented)** The method of claim 57, wherein the lysine is isolated from the cultivation medium.

61. **(Previously Presented)** The method of claim 60, wherein the lysine is purified.

62. **(Previously Presented)** The method of claim 55, wherein the nucleic acid molecule of (1) or the expression unit of (2) alters the expression of the at least one gene.

63. **(Previously Presented)** The method of claim 55, wherein the nucleic acid molecule of (1) or the expression unit of (2) regulates the expression of the at least one gene.

64. **(Previously Presented)** The method of claim 55, wherein the nucleic acid molecule of (1) or the expression unit of (2) causes the expression of the at least one gene.

65. **(Previously Presented)** The method of claim 55, wherein the nucleic acid molecule having promoter activity consists of the nucleotide sequence of SEQ ID NO:1.

66. **(Previously Presented)** The method of claim 55, wherein the expression unit consists of the nucleotide sequence of SEQ ID NO:2.